



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:53 pm GMT

PDB ID : 4BCG  
Title : Structure of CDK9 in complex with cyclin T and a 2-amino-4-heteroaryl-pyrimidine inhibitor  
Authors : Hole, A.J.; Baumli, S.; Wang, S.; Endicott, J.A.; Noble, M.E.M.  
Deposited on : 2012-10-02  
Resolution : 3.08 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

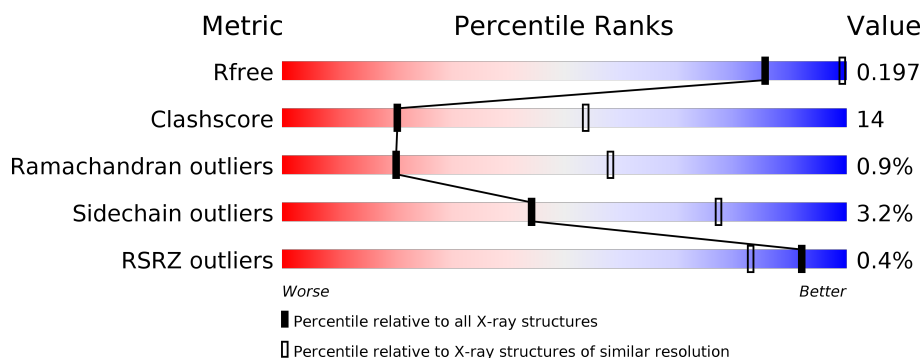
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.08 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	1116 (3.10-3.06)
Clashscore	112137	1220 (3.10-3.06)
Ramachandran outliers	110173	1176 (3.10-3.06)
Sidechain outliers	110143	1176 (3.10-3.06)
RSRZ outliers	101464	1123 (3.10-3.06)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	331	
2	B	260	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	B	1260	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4649 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CYCLIN-DEPENDENT KINASE 9.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	313	2530	1621	437	456	1	15	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	EXPRESSION TAG	UNP P50750
A	1	PRO	-	EXPRESSION TAG	UNP P50750

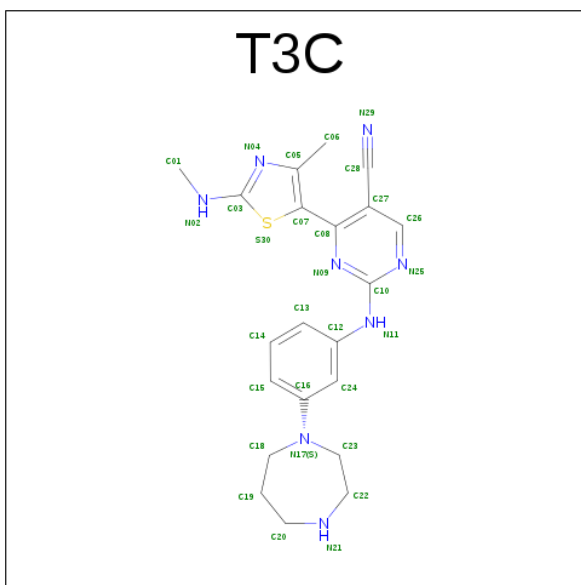
- Molecule 2 is a protein called CYCLIN-T1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	252	2061	1318	360	374	9	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

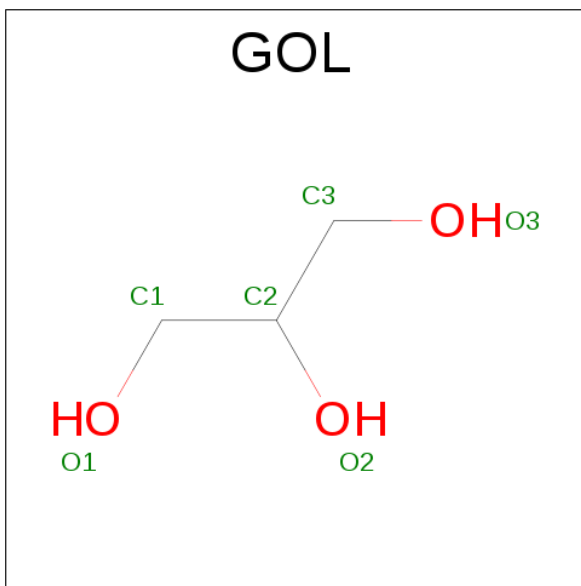
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	EXPRESSION TAG	UNP O60563
B	1	PRO	-	EXPRESSION TAG	UNP O60563
B	77	ARG	GLN	ENGINEERED MUTATION	UNP O60563
B	96	GLY	GLU	ENGINEERED MUTATION	UNP O60563
B	241	LEU	PHE	ENGINEERED MUTATION	UNP O60563

- Molecule 3 is 2-[[3-(1,4-DIAZEPAN-1-YL)PHENYL]AMINO]-4-[4-METHYL-2-(METHYL AMINO)-1,3-THIAZOL-5-YL]PYRIMIDINE-5-CARBONITRILE (three-letter code: T3C) (formula: C<sub>21</sub>H<sub>24</sub>N<sub>8</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	S	0	0
			30	21	8	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

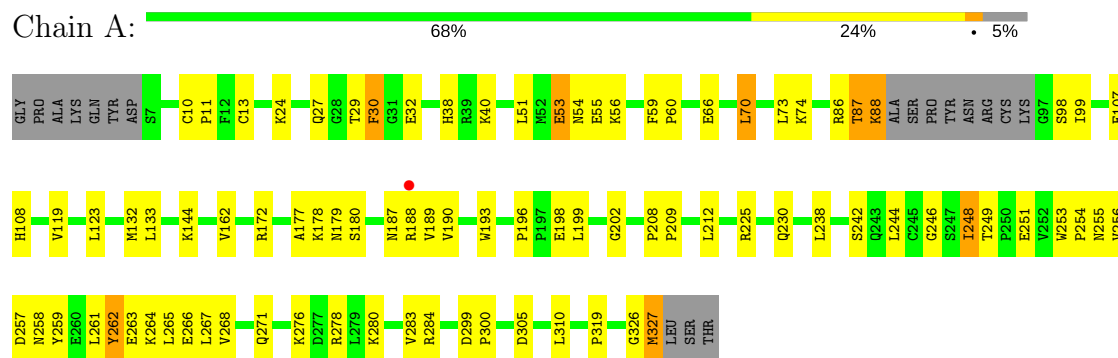
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	7	Total 7	O 7	0	0
5	B	9	Total 9	O 9	0	0

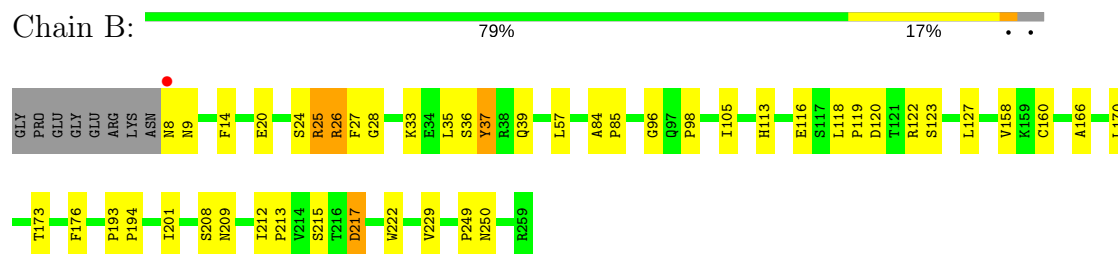
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: CYCLIN-DEPENDENT KINASE 9



#### • Molecule 2: CYCLIN-T1



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	172.80Å 172.80Å 98.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	82.63 – 3.08 82.50 – 3.09	Depositor EDS
% Data completeness (in resolution range)	99.0 (82.63-3.08) 99.0 (82.50-3.09)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 3.07Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.161 , 0.197 0.161 , 0.197	Depositor DCC
$R_{free}$ test set	1023 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	87.0	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 62.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4649	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, GOL, T3C

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.47	0/2569	0.64	0/3465
2	B	0.64	0/2114	0.79	0/2879
All	All	0.55	0/4683	0.71	0/6344

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2530	0	2582	98	0
2	B	2061	0	2049	29	0
3	A	30	0	24	5	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0
5	A	7	0	0	0	0
5	B	9	0	0	0	0
All	All	4649	0	4671	130	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

All (130) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:ILE:HG13	1:A:267:LEU:CD2	1.52	1.40
1:A:177:ALA:CB	1:A:178:LYS:HA	1.58	1.30
1:A:177:ALA:HB1	1:A:178:LYS:HA	1.13	1.06
1:A:248:ILE:HG13	1:A:267:LEU:HD23	1.42	1.02
1:A:248:ILE:HG13	1:A:267:LEU:HD21	1.39	1.01
1:A:257:ASP:HA	1:A:262:TYR:CD2	1.98	0.98
1:A:177:ALA:CB	1:A:178:LYS:CA	2.43	0.96
1:A:249:THR:HG22	1:A:251:GLU:H	1.35	0.89
1:A:253:TRP:O	1:A:256:VAL:HG12	1.72	0.88
1:A:238:LEU:HD13	1:A:265:LEU:CD2	2.04	0.88
1:A:248:ILE:CG1	1:A:267:LEU:CD2	2.48	0.87
1:A:177:ALA:HB3	1:A:178:LYS:HA	1.56	0.85
1:A:196:PRO:HB2	1:A:198:GLU:OE1	1.78	0.82
2:B:25:ARG:O	2:B:28:GLY:N	2.11	0.79
1:A:248:ILE:HG22	1:A:256:VAL:HG21	1.64	0.79
1:A:238:LEU:HD13	1:A:265:LEU:HD22	1.64	0.78
2:B:118:LEU:HD12	2:B:119:PRO:HD2	1.66	0.77
1:A:255:ASN:O	1:A:258:ASN:OD1	2.04	0.76
1:A:257:ASP:HA	1:A:262:TYR:HD2	1.50	0.75
1:A:86:ARG:NH1	1:A:88:LYS:HD3	2.03	0.74
1:A:188:ARG:HD2	1:A:188:ARG:O	1.88	0.74
1:A:179:ASN:O	1:A:180:SER:OG	2.07	0.73
1:A:248:ILE:CG1	1:A:267:LEU:HD21	2.14	0.72
2:B:20:GLU:O	2:B:25:ARG:HG3	1.90	0.72
1:A:86:ARG:HH12	1:A:88:LYS:HD3	1.56	0.69
1:A:177:ALA:HB3	1:A:178:LYS:CA	2.19	0.68
2:B:84:ALA:HB3	2:B:85:PRO:HD3	1.75	0.68
1:A:123:LEU:HD23	1:A:319:PRO:HD2	1.78	0.66
1:A:326:GLY:C	1:A:327:MET:HG3	2.17	0.65
1:A:254:PRO:O	1:A:255:ASN:HB2	1.97	0.65
1:A:268:VAL:HG21	1:A:271:GLN:HG3	1.79	0.64
1:A:238:LEU:HD13	1:A:265:LEU:HD21	1.79	0.64
1:A:24:LYS:HB3	1:A:27:GLN:HE21	1.63	0.64
1:A:55:GLU:CG	1:A:60:PRO:HG3	2.28	0.62
1:A:54:ASN:HB2	1:A:56:LYS:HG3	1.82	0.62
1:A:29:THR:HG21	3:A:1328:T3C:H21	1.65	0.61
1:A:187:ASN:ND2	1:A:202:GLY:HA2	2.16	0.61
1:A:276:LYS:O	1:A:280:LYS:HB2	2.00	0.61
1:A:212:LEU:HD13	1:A:305:ASP:HA	1.81	0.60
2:B:113:HIS:HB3	2:B:116:GLU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:ALA:HB1	1:A:178:LYS:CA	2.07	0.60
1:A:189:VAL:HG23	1:A:199:LEU:HD13	1.83	0.60
2:B:24:SER:O	2:B:25:ARG:C	2.39	0.60
1:A:178:LYS:HG2	1:A:179:ASN:N	2.18	0.59
1:A:248:ILE:CG2	1:A:256:VAL:HG21	2.33	0.59
1:A:248:ILE:HG13	1:A:267:LEU:HD22	1.72	0.59
2:B:24:SER:O	2:B:27:PHE:N	2.35	0.59
1:A:244:LEU:HD13	1:A:278:ARG:HH11	1.68	0.58
1:A:187:ASN:HD21	1:A:202:GLY:HA2	1.68	0.58
2:B:120:ASP:OD2	2:B:122:ARG:HB2	2.03	0.58
1:A:261:LEU:HD23	1:A:264:LYS:HD2	1.84	0.58
1:A:87:THR:CG2	1:A:98:SER:H	2.15	0.57
1:A:38:HIS:CE1	1:A:40:LYS:HB2	2.40	0.56
2:B:208:SER:O	2:B:209:ASN:HB2	2.05	0.56
1:A:262:TYR:CD1	1:A:262:TYR:C	2.80	0.55
2:B:193:PRO:N	2:B:194:PRO:CD	2.70	0.55
2:B:25:ARG:O	2:B:26:ARG:C	2.45	0.55
1:A:283:VAL:O	1:A:284:ARG:HB2	2.07	0.55
2:B:166:ALA:HB1	2:B:170:LEU:HB3	1.89	0.55
1:A:177:ALA:HB3	1:A:178:LYS:CB	2.36	0.55
1:A:29:THR:HG21	3:A:1328:T3C:N21	2.23	0.54
2:B:25:ARG:O	2:B:27:PHE:N	2.40	0.54
1:A:55:GLU:HG2	1:A:60:PRO:HG3	1.88	0.54
1:A:38:HIS:HE1	1:A:40:LYS:HB2	1.73	0.54
1:A:87:THR:HG21	1:A:98:SER:H	1.72	0.54
1:A:53:GLU:O	1:A:54:ASN:CG	2.46	0.54
1:A:178:LYS:O	1:A:179:ASN:HB2	2.09	0.53
1:A:87:THR:O	1:A:88:LYS:CB	2.56	0.53
1:A:73:LEU:O	1:A:74:LYS:HD3	2.08	0.53
1:A:54:ASN:HA	1:A:55:GLU:C	2.29	0.52
1:A:262:TYR:HD1	1:A:262:TYR:C	2.12	0.52
1:A:132:MET:CE	1:A:162:VAL:HA	2.39	0.52
1:A:248:ILE:CG1	1:A:267:LEU:HD23	2.27	0.52
1:A:107:GLU:HG3	1:A:108:HIS:CE1	2.45	0.51
1:A:242:SER:OG	1:A:267:LEU:HD11	2.11	0.51
1:A:51:LEU:HD22	1:A:51:LEU:N	2.26	0.51
1:A:66:GLU:HG2	1:A:70:LEU:HD22	1.92	0.51
1:A:263:GLU:OE1	1:A:263:GLU:HA	2.11	0.50
1:A:10:CYS:N	1:A:11:PRO:HD3	2.27	0.50
1:A:242:SER:HA	1:A:246:GLY:O	2.11	0.50
1:A:86:ARG:HH12	1:A:88:LYS:CD	2.23	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:96:GLY:C	2:B:98:PRO:HD3	2.32	0.50
1:A:87:THR:CG2	1:A:88:LYS:N	2.75	0.50
1:A:265:LEU:CD2	1:A:267:LEU:HB2	2.41	0.50
1:A:30:PHE:CD1	1:A:30:PHE:N	2.80	0.50
2:B:36:SER:O	2:B:37:TYR:C	2.48	0.50
3:A:1328:T3C:H24	3:A:1328:T3C:N09	2.27	0.49
1:A:24:LYS:HB3	1:A:27:GLN:NE2	2.26	0.49
1:A:187:ASN:OD1	1:A:187:ASN:O	2.30	0.49
1:A:10:CYS:SG	1:A:13:CYS:HB3	2.53	0.49
1:A:178:LYS:HG2	1:A:179:ASN:H	1.78	0.48
2:B:166:ALA:CB	2:B:170:LEU:HD23	2.44	0.47
2:B:217:ASP:OD1	2:B:217:ASP:N	2.48	0.47
3:A:1328:T3C:C28	3:A:1328:T3C:H061	2.46	0.46
1:A:259:TYR:C	1:A:261:LEU:H	2.20	0.46
2:B:36:SER:O	2:B:39:GLN:N	2.48	0.46
1:A:132:MET:HE1	1:A:162:VAL:HA	1.96	0.46
1:A:208:PRO:N	1:A:209:PRO:CD	2.79	0.45
2:B:120:ASP:O	2:B:123:SER:OG	2.24	0.45
1:A:133:LEU:HD23	1:A:133:LEU:C	2.37	0.45
1:A:144:LYS:HD3	1:A:144:LYS:HA	1.73	0.45
2:B:57:LEU:HD12	2:B:57:LEU:O	2.17	0.45
1:A:268:VAL:HG21	1:A:271:GLN:CG	2.44	0.45
1:A:265:LEU:HD23	1:A:267:LEU:HB2	1.98	0.45
1:A:299:ASP:HA	1:A:300:PRO:HD2	1.83	0.44
1:A:59:PHE:HA	1:A:60:PRO:HD3	1.87	0.44
2:B:249:PRO:O	2:B:250:ASN:HB2	2.17	0.44
1:A:249:THR:HG22	1:A:251:GLU:N	2.18	0.44
1:A:249:THR:HG22	1:A:251:GLU:HB3	2.00	0.44
1:A:249:THR:CG2	1:A:251:GLU:HB3	2.48	0.43
2:B:8:ASN:HB3	2:B:9:ASN:H	1.62	0.43
1:A:86:ARG:NH1	1:A:88:LYS:CD	2.78	0.43
2:B:212:ILE:HA	2:B:213:PRO:HD3	1.90	0.43
1:A:267:LEU:HD12	1:A:268:VAL:H	1.84	0.43
1:A:119:VAL:O	1:A:225:ARG:NH2	2.45	0.43
1:A:55:GLU:HG3	1:A:60:PRO:HG3	2.00	0.43
1:A:261:LEU:HD23	1:A:261:LEU:HA	1.85	0.43
1:A:244:LEU:HD13	1:A:278:ARG:NH1	2.34	0.42
1:A:193:TRP:CD1	1:A:230:GLN:HA	2.54	0.42
2:B:166:ALA:HB1	2:B:170:LEU:HD23	2.02	0.42
2:B:14:PHE:CD1	2:B:14:PHE:N	2.88	0.42
1:A:86:ARG:HA	1:A:99:ILE:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:173:THR:O	2:B:176:PHE:HB3	2.20	0.41
1:A:30:PHE:HD1	1:A:30:PHE:N	2.18	0.41
1:A:248:ILE:HG23	1:A:253:TRP:CE3	2.56	0.41
2:B:127:LEU:HD23	2:B:127:LEU:HA	1.82	0.41
2:B:222:TRP:CD1	2:B:229:VAL:HG12	2.56	0.41
3:A:1328:T3C:C28	3:A:1328:T3C:C06	2.98	0.41
1:A:310:LEU:HA	1:A:310:LEU:HD23	1.87	0.41
2:B:160:CYS:SG	2:B:201:ILE:HD13	2.61	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	308/331 (93%)	281 (91%)	26 (8%)	1 (0%)	44	78
2	B	250/260 (96%)	240 (96%)	6 (2%)	4 (2%)	11	42
All	All	558/591 (94%)	521 (93%)	32 (6%)	5 (1%)	20	58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	190	VAL
2	B	26	ARG
2	B	215	SER
2	B	37	TYR
2	B	158	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	276/291 (95%)	265 (96%)	11 (4%)	36	72
2	B	230/236 (98%)	225 (98%)	5 (2%)	57	84
All	All	506/527 (96%)	490 (97%)	16 (3%)	44	77

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	PHE
1	A	32	GLU
1	A	53	GLU
1	A	70	LEU
1	A	87	THR
1	A	88	LYS
1	A	172	ARG
1	A	248	ILE
1	A	262	TYR
1	A	266	GLU
1	A	327	MET
2	B	25	ARG
2	B	33	LYS
2	B	35	LEU
2	B	105	ILE
2	B	217	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	108	HIS
1	A	187	ASN
1	A	232	ASN
1	A	258	ASN
2	B	239	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	TPO	A	186	1	9,10,11	0.88	0	10,14,16	1.49	2 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	A	186	1	-	0/8/11/13	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	TPO	O-C-CA	-2.11	120.22	125.15
1	A	186	TPO	O2P-P-O1P	2.01	118.37	110.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	T3C	A	1328	-	24,33,33	2.10	9 (37%)	25,45,45	2.15	6 (24%)
4	GOL	A	1329	-	5,5,5	0.35	0	5,5,5	0.85	0
4	GOL	B	1260	-	5,5,5	0.39	0	5,5,5	0.35	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	T3C	A	1328	-	-	0/9/25/25	1/4/4/4
4	GOL	A	1329	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1260	-	-	0/4/4/4	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1328	T3C	C08-C07	-4.29	1.39	1.49
3	A	1328	T3C	C23-N17	-2.31	1.43	1.46
3	A	1328	T3C	C08-N09	2.10	1.37	1.34
3	A	1328	T3C	C06-C05	2.27	1.54	1.50
3	A	1328	T3C	C10-N25	2.44	1.37	1.34
3	A	1328	T3C	C27-C28	2.65	1.48	1.44
3	A	1328	T3C	C13-C12	2.78	1.43	1.39
3	A	1328	T3C	C16-N17	3.45	1.48	1.38
3	A	1328	T3C	C10-N11	5.31	1.46	1.36



All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1328	T3C	C01-N02-C03	-6.23	117.52	122.85
3	A	1328	T3C	N25-C10-N09	-5.15	121.73	126.68
3	A	1328	T3C	C15-C16-N17	-2.87	117.36	121.39
3	A	1328	T3C	C27-C26-N25	-2.18	120.06	123.39
3	A	1328	T3C	C26-N25-C10	2.39	119.83	115.88
3	A	1328	T3C	C07-C08-N09	2.98	118.78	114.97

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1328	T3C	C18-C19-C20-C22-C23-N17-N21

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1328	T3C	5	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	312/331 (94%)	0.02	1 (0%) 93 85	51, 90, 161, 211	0
2	B	252/260 (96%)	0.00	1 (0%) 92 83	50, 75, 132, 181	0
All	All	564/591 (95%)	0.01	2 (0%) 92 83	50, 83, 152, 211	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	8	ASN	3.5
1	A	188	ARG	2.3

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	TPO	A	186	11/12	0.95	0.20	-	75,87,101,101	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	B	1260	6/6	0.88	0.30	2.57	86,87,98,100	0
3	T3C	A	1328	30/30	0.97	0.32	1.69	61,80,147,163	0
4	GOL	A	1329	6/6	0.87	0.30	1.68	83,93,99,119	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.